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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/845,335

DATE: 12/26/2001

TIME: 15:50:36

Input Set : N:\Crif3\RULE60\09845335.raw

Output Set: N:\CRF3\12262001\I845335.raw

1 <110> APPLICANT: CLOUGH, BARBARA  
 2 PREISER, PETER  
 3 WILSON, ROBERT  
 4 <120> TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE  
 5 MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS  
 6 EFFECTIVE AS ANTI-MALARIAL COMPOUNDS  
 7 <130> FILE REFERENCE: N68837B GCW PJC DP  
 8 <140> CURRENT APPLICATION NUMBER: 09/845,335  
 9 <141> CURRENT FILING DATE: 2001-12-26  
 10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/140,466  
 W--> 11 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-26  
 12 <160> NUMBER OF SEQ ID NOS: 14  
 13 <170> SOFTWARE: PatentIn Ver. 2.1  
 15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 1230  
 17 <212> TYPE: DNA  
 18 <213> ORGANISM: Plasmodium falciparum  
 19 <220> FEATURE:  
 20 <221> NAME/KEY: CDS  
 21 <222> LOCATION: (1)..(1230)  
 22 <400> SEQUENCE: 1  
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 24 Met Asn Asn Lys Leu Phe Leu Arg Asn Lys Gln His Ile Asn Leu Gly  
 25 1 5 10 15  
 26 act ata ggg cat gta gat cat gga aaa act aca tta aca aca gct ata 96  
 27 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Thr Ala Ile  
 28 20 25 30  
 29 tct tat tta tta aat tta caa gga tta tca aaa aaa tat aat tat tca 144  
 30 Ser Tyr Leu Leu Asn Leu Gln Gly Leu Ser Lys Lys Tyr Asn Tyr Ser  
 31 35 40 45  
 32 gat att gat tca gct cca gaa gaa aaa ata aga ggt att aca ata aat 192  
 33 Asp Ile Asp Ser Ala Pro Glu Glu Lys Ile Arg Gly Ile Thr Ile Asn  
 34 50 55 60  
 35 aca aca cat att gaa tat gaa act tta aca aaa cat tgt gct cat ata 240  
 36 Thr Thr His Ile Glu Tyr Glu Thr Leu Thr Lys His Cys Ala His Ile  
 37 65 70 75 80  
 38 gat tgt cca gga cat tcc gat tat att aaa aat atg att ata gga gcc 288  
 39 Asp Cys Pro Gly His Ser Asp Tyr Ile Lys Asn Met Ile Ile Gly Ala  
 40 85 90 95  
 41 aca caa atg gat ata gca att tta gta ata tct ata ata gat ggt ata 336  
 42 Thr Gln Met Asp Ile Ala Ile Leu Val Ile Ser Ile Ile Asp Gly Ile  
 43 100 105 110  
 44 atg cct caa act tat gaa cat tta tta tta ata aaa caa ata ggt ata 384  
 45 Met Pro Gln Thr Tyr Glu His Leu Leu Leu Ile Lys Gln Ile Gly Ile  
 46 115 120 125  
 47 aaa aat ata att att ttt tta aat aaa gaa gat tta tgt gat gat gtt 432  
 48 Lys Asn Ile Ile Ile Phe Leu Asn Lys Glu Asp Leu Cys Asp Asp Val

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49	130	135	140	
50	gaa tta ata gat ttt ata aaa tta gaa gta aat gaa tta tta att aaa	480		
51	Glu Leu Ile Asp Phe Ile Lys Leu Glu Val Asn Glu Leu Leu Ile Lys			
52	145 150 155 160			
53	tat aat ttt gat tta aat tat ata cat ata tta act ggt tca gca tta	528		
54	Tyr Asn Phe Asp Leu Asn Tyr Ile His Ile Leu Thr Gly Ser Ala Leu			
55	165 170 175			
56	aat gta ata aat ata att caa aaa aat aag gat tat gaa tta ata aaa	576		
57	Asn Val Ile Asn Ile Ile Gln Lys Asn Lys Asp Tyr Glu Leu Ile Lys			
58	180 185 190			
59	tct aat att tgg ata caa aaa tta aat aat tta att caa ata att gat	624		
60	Ser Asn Ile Trp Ile Gln Lys Leu Asn Asn Leu Ile Gln Ile Ile Asp			
61	195 200 205			
62	aat att ata ata cct act aga aaa att aat gat tac ttt tta atg tca	672		
63	Asn Ile Ile Ile Pro Thr Arg Lys Ile Asn Asp Tyr Phe Leu Met Ser			
64	210 215 220			
65	ata gaa gat gta ttt tct ata aca ggt aga ggt aca gta gta aca ggt	720		
66	Ile Glu Asp Val Phe Ser Ile Thr Gly Arg Gly Thr Val Val Thr Gly			
67	225 230 235 240			
68	aag att gaa caa gga tgt ata aat tta aat gat gaa att gaa att tta	768		
69	Lys Ile Glu Gln Gly Cys Ile Asn Leu Asn Asp Glu Ile Glu Ile Leu			
70	245 250 255			
71	aaa ttt gaa aaa tca tct cct aat tta aca aca gtt ata gga tta gaa	816		
72	Lys Phe Glu Lys Ser Ser Pro Asn Leu Thr Thr Val Ile Gly Leu Glu			
73	260 265 270			
74	atg ttt aaa aaa caa tta aca caa gca caa tcc gga gat aat gta ggt	864		
75	Met Phe Lys Lys Gln Leu Thr Gln Ala Gln Ser Gly Asp Asn Val Gly			
76	275 280 285			
77	att tta tta aga aat att caa aaa aaa gat ata aaa aga ggt atg att	912		
78	Ile Leu Leu Arg Asn Ile Gln Lys Lys Asp Ile Lys Arg Gly Met Ile			
79	290 295 300			
80	tta gca aca cct aat aaa tta aaa gta tat aag tct ttt ata gct gaa	960		
81	Leu Ala Thr Pro Asn Lys Leu Lys Val Tyr Lys Ser Phe Ile Ala Glu			
82	305 310 315 320			
83	aca tat att tta act aaa gaa gaa ggt ggt cgt cat aaa cct ttt aat	1008		
84	Thr Tyr Ile Leu Thr Lys Glu Glu Gly Gly Arg His Lys Pro Phe Asn			
85	325 330 335			
86	att gga tat aaa cct caa ttt ttt att cgt aca gta gat gtt act gga	1056		
87	Ile Gly Tyr Lys Pro Gln Phe Phe Ile Arg Thr Val Asp Val Thr Gly			
88	340 345 350			
89	gaa att aaa aat ata tat tta aat gaa aat gta caa aaa gta gct ata	1104		
90	Glu Ile Lys Asn Ile Tyr Leu Asn Glu Asn Val Gln Lys Val Ala Ile			
91	355 360 365			
92	cct gga gat aaa ata aca tta cat att gaa tta aaa cat tat ata gtg	1152		
93	Pro Gly Asp Lys Ile Thr Leu His Ile Glu Leu Lys His Tyr Ile Val			
94	370 375 380			
95	ttg aca tta aat atg aaa ttt tct att aga gaa gga gga aaa aca ata	1200		
96	Leu Thr Leu Asn Met Lys Phe Ser Ile Arg Glu Gly Gly Lys Thr Ile			
97	385 390 395 400			

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102 <210> SEQ ID NO: 2
103 <211> LENGTH: 410
104 <212> TYPE: PRT
105 <213> ORGANISM: Plasmodium falciparum
106 <400> SEQUENCE: 2
107      Met Asn Asn Lys Leu Phe Leu Arg Asn Lys Gln His Ile Asn Leu Gly
108      1             5             10             15
109      Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Thr Ala Ile
110             20             25             30
111      Ser Tyr Leu Leu Asn Leu Gln Gly Leu Ser Lys Lys Tyr Asn Tyr Ser
112             35             40             45
113      Asp Ile Asp Ser Ala Pro Glu Glu Lys Ile Arg Gly Ile Thr Ile Asn
114      50             55             60
115      Thr Thr His Ile Glu Tyr Glu Thr Leu Thr Lys His Cys Ala His Ile
116      65             70             75             80
117      Asp Cys Pro Gly His Ser Asp Tyr Ile Lys Asn Met Ile Ile Gly Ala
118             85             90             95
119      Thr Gln Met Asp Ile Ala Ile Leu Val Ile Ser Ile Ile Asp Gly Ile
120             100            105            110
121      Met Pro Gln Thr Tyr Glu His Leu Leu Leu Ile Lys Gln Ile Gly Ile
122             115            120            125
123      Lys Asn Ile Ile Ile Phe Leu Asn Lys Glu Asp Leu Cys Asp Asp Val
124      130            135            140
125      Glu Leu Ile Asp Phe Ile Lys Leu Glu Val Asn Glu Leu Leu Ile Lys
126      145            150            155            160
127      Tyr Asn Phe Asp Leu Asn Tyr Ile His Ile Leu Thr Gly Ser Ala Leu
128             165            170            175
129      Asn Val Ile Asn Ile Ile Gln Lys Asn Lys Asp Tyr Glu Leu Ile Lys
130             180            185            190
131      Ser Asn Ile Trp Ile Gln Lys Leu Asn Asn Leu Ile Gln Ile Ile Asp
132             195            200            205
133      Asn Ile Ile Ile Pro Thr Arg Lys Ile Asn Asp Tyr Phe Leu Met Ser
134      210            215            220
135      Ile Glu Asp Val Phe Ser Ile Thr Gly Arg Gly Thr Val Val Thr Gly
136      225            230            235            240
137      Lys Ile Glu Gln Gly Cys Ile Asn Leu Asn Asp Glu Ile Glu Ile Leu
138             245            250            255
139      Lys Phe Glu Lys Ser Ser Pro Asn Leu Thr Thr Val Ile Gly Leu Glu
140             260            265            270
141      Met Phe Lys Lys Gln Leu Thr Gln Ala Gln Ser Gly Asp Asn Val Gly
142             275            280            285
143      Ile Leu Leu Arg Asn Ile Gln Lys Lys Asp Ile Lys Arg Gly Met Ile
144      290            295            300
145      Leu Ala Thr Pro Asn Lys Leu Lys Val Tyr Lys Ser Phe Ile Ala Glu
146      305            310            315            320
147      Thr Tyr Ile Leu Thr Lys Glu Glu Gly Gly Arg His Lys Pro Phe Asn

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148          325          330          335
149   Ile Gly Tyr Lys Pro Gln Phe Phe Ile Arg Thr Val Asp Val Thr Gly
150          340          345          350
151   Glu Ile Lys Asn Ile Tyr Leu Asn Glu Asn Val Gln Lys Val Ala Ile
152          355          360          365
153   Pro Gly Asp Lys Ile Thr Leu His Ile Glu Leu Lys His Tyr Ile Val
154          370          375          380
155   Leu Thr Leu Asn Met Lys Phe Ser Ile Arg Glu Gly Gly Lys Thr Ile
156          385          390          395          400
157   Gly Ala Gly Ile Ile Thr Glu Ile Lys Asn
158          405          410
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 409
162 <212> TYPE: PRT
163 <213> ORGANISM: Anacystis nidulans
164 <400> SEQUENCE: 3
165   Met Ala Arg Ala Lys Phe Glu Arg Thr Lys Pro His Ala Asn Ile Gly
166     1          5          10          15
167   Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
168          20          25          30
169   Thr Thr Val Leu Ala Lys Ala Gly Met Ala Lys Ala Arg Ala Tyr Ala
170          35          40          45
171   Asp Ile Asp Ala Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
172          50          55          60
173   Thr Ala His Val Glu Tyr Glu Thr Gly His Arg His Tyr Ala His Val
174          65          70          75          80
175   Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
176          85          90          95
177   Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Ala Asp Gly Pro
178          100         105         110
179   Met Pro Gln Thr Arg Glu His Ile Leu Leu Ala Lys Gln Val Gly Val
180          115         120         125
181   Pro Asn Ile Val Val Phe Leu Asn Lys Glu Asp Met Val Asp Asp Ala
182          130         135         140
183   Glu Leu Leu Glu Leu Val Glu Leu Glu Val Arg Glu Leu Leu Ser Ser
184          145         150         155         160
185   Tyr Asp Phe Pro Gly Asp Asp Ile Pro Ile Val Ala Gly Ser Ala Leu
186          165         170         175
187   Gln Ala Leu Glu Ala Ile Gln Gly Gly Ala Ser Gly Gln Lys Gly Asp
188          180         185         190
189   Asn Pro Trp Val Asp Lys Ile Leu Lys Leu Met Glu Glu Val Asp Ala
190          195         200         205
191   Tyr Ile Pro Thr Pro Glu Arg Glu Val Asp Arg Pro Phe Leu Met Ala
192          210         215         220
193   Val Glu Asp Val Phe Thr Ile Thr Gly Arg Gly Thr Val Ala Thr Gly
194          225         230         235         240
195   Arg Ile Glu Arg Gly Ser Val Lys Val Gly Glu Thr Ile Glu Ile Val
196          245         250         255
197   Gly Leu Arg Asp Thr Arg Ser Thr Thr Val Thr Gly Val Glu Met Phe

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198          260          265          270
199  Gln Lys Thr Leu Asp Glu Gly Leu Ala Gly Asp Asn Val Gly Leu Leu
200          275          280          285
201  Leu Arg Gly Ile Gln Lys Thr Asp Ile Glu Arg Gly Met Val Leu Ala
202          290          295          300
203  Lys Pro Gly Ser Ile Thr Pro His Thr Lys Phe Glu Ser Glu Val Tyr
204          305          310          315          320
205  Val Leu Lys Lys Glu Glu Gly Gly Arg His Thr Pro Phe Phe Pro Gly
206          325          330          335
207  Tyr Arg Pro Gln Phe Tyr Val Arg Thr Thr Asp Val Thr Gly Ala Ile
208          340          345          350
209  Ser Asp Phe Thr Ala Asp Asp Gly Ser Ala Ala Glu Met Val Ile Pro
210          355          360          365
211  Gly Asp Arg Ile Lys Met Thr Val Glu Leu Ile Asn Pro Ile Ala Ile
212          370          375          380
213  Glu Gln Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile Gly
214          385          390          395          400
215  Ala Gly Val Val Ser Lys Ile Leu Gln
216          405
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 408
220 <212> TYPE: PRT
221 <213> ORGANISM: Cryptomonas phi
222 <400> SEQUENCE: 4
223  Met Ala Arg Asp Lys Phe Glu Arg Ser Lys Pro His Val Asn Ile Gly
224    1          5          10          15
225  Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
226          20          25          30
227  Ser Ala Thr Leu Ser Gln Tyr Thr Gly Lys Ser Lys Lys Phe Asp Glu
228          35          40          45
229  Ile Asp Ser Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn Thr
230          50          55          60
231  Ala His Val Glu Tyr Glu Thr Asp Lys Trp Tyr Tyr Ala His Val Asp
232          65          70          75          80
233  Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala Ala
234          85          90          95
235  Gln Met Asp Gly Ala Ile Leu Val Cys Ser Ala Ala Asn Gly Pro Met
236          100          105          110
237  Pro Gln Thr Arg Glu His Ile Leu Leu Ala Lys Gln Val Gly Val Pro
238          115          120          125
239  Tyr Ile Val Val Phe Leu Asn Lys Ala Asp Met Val Asp Asp Glu Glu
240          130          135          140
241  Leu Leu Glu Leu Val Gln Leu Glu Val Gln Glu Leu Leu Glu Lys Tyr
242          145          150          155          160
243  Asp Phe Pro Gly Ser Glu Ile Pro Phe Val Ala Gly Ser Ala Leu Leu
244          165          170          175
245  Ala Leu Glu Ala Val Ala Asn Asn Pro Thr Ile Lys Arg Gly Glu Asp
246          180          185          190
247  Lys Trp Val Asp Thr Ile Tyr Gln Leu Met Asp Lys Val Asp Glu Tyr

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VERIFICATION SUMMARY

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